15. Progress towards Molecular Breeding of Switchgrass for Feedstock Yield and Quality

Desalegn D. Serba[1,2*] (ddserba@noble.org), Malay C. Saha,[1,2] Ananta Acharya,[1,2,3] Jeremy Schmutz,[4,5] Angela Ziebell,[1,6†] Erica Gjersing,[1,6] Robert Sykes,[1,6] Joe H. Bouton,[1,2,3] Katrien M. Devos,[1,3] E. Charles Brummer,[1,2‡] and Paul Gilna[1]

[1]BioEnergy Science Center, Oak Ridge National Laboratory, Oak Ridge, Tennessee; [2] The Samuel Roberts Noble Foundation, Ardmore, Oklahoma; [3]University of Georgia, Athens; [4]Joint Genome Institute, Walnut Creek, California; [5]Hudson Alpha Institute for Biotechnology, Huntsville, Alabama; [6]National Renewable Energy Laboratory, Golden, Colorado

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Project Goals: The BioEnergy Science Center (BESC) is focused on the fundamental understanding and elimination of biomass recalcitrance. BESC's approach to improve accessibility to the sugars within biomass involves (1) designing plant cell walls for rapid deconstruction and (2) developing multi-talented microbes or converting plant biomass into biofuels in a single step (consolidated bioprocessing). BESC biomass formation and modification research involves working directly with two potential bioenergy crops (switchgrass and Populus) to develop varieties that are easier to break down into fermentable sugars. We are using both testing and generating tools for detailed studies into poorly understood cell wall biosynthesis pathways.

Improved biomass yield and reduced recalcitrance are the two key breeding goals for switchgrass (Panicum virgatum L.), a second-generation biofuel feedstock. Application of molecular techniques facilitates the breeding process and also improves the selection efficiency per cycle. Linkage map of AP13 (lowland) consisting of 515 loci arranged in 18 linkage groups spanning 1,733 cM; and VS16 (upland) consisting 363 loci arranged in 17 linkage groups spanning 1,508 cM were constructed. Quantitative trait loci (QTL) analysis using phenotypic data from multiple environments identified 11 genomic regions controlling both biomass yield and plant height traits. Similarly, 9 and 14 genomic regions were identified controlling sugar release and lignin content, respectively. Both the yield and quality traits are controlled by several QTL of minor effects each. An association mapping population (AMP) consisting of 480 genotypes from 36 accessions mainly collected from the southern United States has been phenotyped at two environments in Georgia and Oklahoma. Significant variation was observed for lignin content (18.3 to 28.0% of dry matter) and total sugar (glucose + xylose) release (245–571 mg g-1). Genotyping by sequencing of 352 of the AMP panels with FseI-MspI identified over 65,000 single nucleotide polymorphisms (SNPs).

Structure analysis distinguished distinct ecotype groups and sub-groups within each ecotype. A subset of 3,196 SNPs that could be genotyped in at least 80% of population was used in preliminary marker-trait associations for biomass yield, plant height, stem thickness, and days to flower. After correction for false discovery, 51 SNPs were found associated with the four traits. Three of the SNPs were associated with both plant height and biomass yield. To generate more markers, genotyping of the population with exome capture is in progress. Based on sugar release, biomass yield, and lignin content six genotypes were identified from the AMP. Two of these genotypes that exhibit both reduced recalcitrance and high biomass yield are currently under further field and greenhouse evaluations.

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